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PATENT  
Docket No.: 201040/1020

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) :	Alam et al.	)	Examiner:	
Serial No. :	09/455,978	)	H. Schnizer	
Cnfrm. No. :	5811	)	Art Unit:	
Filed :	December 6, 1999	)	1653	
For :	HEME PROTEINS HEMAT-HS AND HEMAT-BS AND THEIR USE IN MEDICINE AND MICROSENSORS	)		

Commissioner for Patents  
Washington, D.C. 20231  
Box: SEQUENCE

BEST AVAILABLE COPY

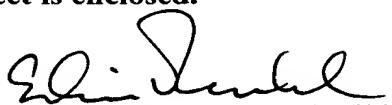
Dear Sir:

Transmitted herewith in the above-identified application are:

- Request for One-Month Extension of Time.
  - Statement in Accordance with 37 C.F.R. § 1.821(g), Sequence Listing (38 pages), and computer readable 3.5" Diskette.
  - Copy of Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures and Raw Sequence Listing Error Report; and
  - A self-addressed postcard for acknowledging receipt.
- The Commissioner is hereby authorized to charge any additional fees or credit any overpayment to Deposit Account No. 14-1138.

A duplicate copy of this sheet is enclosed.

Date: October 23, 2001

  
Edwin V. Merkel  
Registration No. 40,087

Nixon Peabody LLP  
Clinton Square, P.O. Box 31051  
Rochester, New York 14603-1051  
Telephone: (716) 263-1128  
Facsimile: (716) 263-1600

RS29962.1

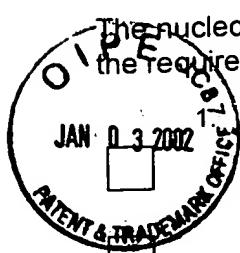
Certificate of Mailing - 37 CFR 1.8(a)

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231, on the date below.

10/23/01 | Jo Ann Whalen  
Date | Jo Ann Whalen

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).



The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g).

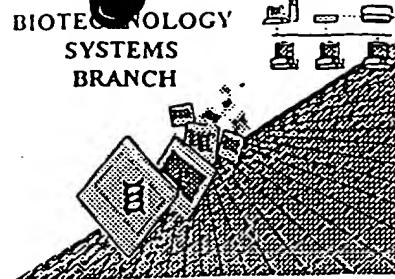
For questions regarding compliance to these requirements, please contact:

- For Rules Interpretation, call (703) 308-4216 or (703) 308-2923
- For CRF Submission Help, call (703) 308-4212
- For PatentIn software Program Support:
  - HELP DESK: (703) 739-8559, ext 508, M-F, 8 AM to 5 PM EST except holidays
  - Email: [PATIN21HELP@uspto.gov](mailto:PATIN21HELP@uspto.gov)
  - To purchase PatentIn software: (703) 306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

*H. Schrizer*

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 69/455, 978  
Source: OIPR  
Date Processed by STIC: 7/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>



## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/455,978</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPIIA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	

Rerun



OPIE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001  
TIME: 13:15:00

Input Set : A:\H1020011.app  
Output Set: N:\CRF3\07062001\I455978.raw

3 <110> APPLICANT: Alam, Maqsudul  
4 Larsen, Randy  
6 <120> TITLE OF INVENTION: HEME PROTEINS HEMAT-HS AND HEMAT-BS AND THEIR USE IN  
7 MEDICINE AND MICROSENSORS  
9 <130> FILE REFERENCE: 201040/1020  
11 <140> CURRENT APPLICATION NUMBER: 09/455,978  
12 <141> CURRENT FILING DATE: 1999-12-06  
14 <160> NUMBER OF SEQ ID NOS: 86  
16 <170> SOFTWARE: PatentIn Ver. 2.1  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 1470  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Halobacterium salinarum  
23 <400> SEQUENCE: 1  
24 atgagcaacg ataatgacac tctcggtacc gcccacgttc ggaacgggat cgacgggcac 60  
25 gcactcgcgg accggatcg cctcgacgag gcgaggatcg cgtggcggtc gtcgttccacc 120  
26 gggatcgcacg acgacacatggccgcgtc gcccggaaac agccgctttt cgaagccacc 180  
27 gcgacgcgc tggtgaccga ctcttacgac cacttggagt cctacgagcg cacacaggac 240  
28 ctcttcgaga actccacgaa gaccgtcgag caactcaaag agacgcaggc cgagtacttg 300  
29 ctggcctcg ggcgcggcga gtacgacacc gagtaacgc cccagcgcgc ccgtatcggg 360  
30 aagatacacg acgtgctcgg gctcggaccg gacgtctatc tggcgcgta cacgcgatac 420  
31 tacacggggc tggggacgc gcttgcgcac gacgtgtcg ccgaccgcgg cgaggaggcg 480  
32 gcccgcggc tcgacgaaact cgtggcccg ttcctgcga tggtaagct gttgacattc 540  
33 gatcagcaga tcgcaatggc cacatcact gactcgatc cccagcgcct ccacgacgag 600  
34 atcgacagcc gcccaggatg ggcgaacgcg gtcgcacgc acgtgaaagc accgtgtcc 660  
35 tcgctggagg cgacctcgca ggacgtcgcc gagcgacagg acacgatgcg gcccgcacc 720  
36 gacgaccagg tcgaccgcat ggctgacgtc agccgtgaga tatccagct gtccgcgagc 780  
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38 ctggcccgac agggcgaggc ggccgcgcac gacgcgtcg ccacgatgac cgacatcgac 900  
39 gaggcgaccg acggcgatc cgcggcggtc gaacagctcg gcgagcgcgc cgccgacgtc 960  
40 gaatcagtga cccgcgtatcg acgtgacatc gccgagcaga cgaacatgtc ggctgtgaa 1020  
41 gctccatcg agggcgcccg cgccggggag gccccggagg gtttgcggt cgtcgccgac 1080  
42 gaggtcaagg ccctcgccga ggagtccgcg gagcgttca cgcgcgtcg ggagctgtc 1140  
43 gagcagatgc aggccggagac cgaggagacg gtcgaccagt tggacgagggt caaccagcgc 1200  
44 atcgcgagg gctcgagcg cgtcgaggag gctgtggaga ccctccaggaa gatcaccgac 1260  
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46 gtgagcaccg aggaggctcg ctagatggtc gacgggtgtcg acgaccgcgc gggcgagatc 1380  
47 gcccgcggcc tcgatgacat cgccgacgac accgatcagc aggtccggac cgtcgaggag 1440  
48 gtccgcgaga cggtcggcaa gtcagctag 1470

Does Not Comply  
Corrected Diskette Needed

see page 5

51 <210> SEQ ID NO: 2  
52 <211> LENGTH: 489  
53 <212> TYPE: PRT  
54 <213> ORGANISM: Halobacterium salinarum  
56 <400> SEQUENCE: 2  
57 Met Ser Asn Asp Asn Asp Thr Leu Val Thr Ala Asp Val Arg Asn Gly  
58 1 5 10 15  
60 Ile Asp Gly His Ala Leu Ala Asp Arg Ile Gly Leu Asp Glu Ala Glu

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001  
TIME: 13:15:00

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Output Set: N:\CRF3\07062001\I455978.raw

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63	Ile Ala Trp Arg Leu Ser Phe Thr Gly Ile Asp Asp Asp Thr Met Ala			
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66	Ala Leu Ala Ala Glu Gln Pro Leu Phe Glu Ala Thr Ala Asp Ala Leu			
67	50	55	60	
69	Val Thr Asp Phe Tyr Asp His Leu Glu Ser Tyr Glu Arg Thr Gln Asp			
70	65	70	75	80
72	Leu Phe Ala Asn Ser Thr Lys Thr Val Glu Gln Leu Lys Glu Thr Gln			
73	85	90	95	
75	Ala Glu Tyr Leu Leu Gly Leu Gly Arg Gly Glu Tyr Asp Thr Glu Tyr			
76	100	105	110	
78	Ala Ala Gln Arg Ala Arg Ile Gly Lys Ile His Asp Val Leu Gly Leu			
79	115	120	125	
81	Gly Pro Asp Val Tyr Leu Gly Ala Tyr Thr Arg Tyr Tyr Thr Gly Leu			
82	130	135	140	
84	Leu Asp Ala Leu Ala Asp Asp Val Val Ala Asp Arg Gly Glu Glu Ala			
85	145	150	155	160
87	Ala Ala Ala Val Asp Glu Leu Val Ala Arg Phe Leu Pro Met Leu Lys			
88	165	170	175	
90	Leu Leu Thr Phe Asp Gln Gln Ile Ala Met Asp Thr Tyr Ile Asp Ser			
91	180	185	190	
93	Tyr Ala Gln Arg Leu His Asp Glu Ile Asp Ser Arg Gln Glu Leu Ala			
94	195	200	205	
96	Asn Ala Val Ala Thr His Val Glu Ala Pro Leu Ser Ser Leu Glu Ala			
97	210	215	220	
99	Thr Ser Gln Asp Val Ala Glu Arg Thr Asp Thr Met Arg Ala Arg Thr			
100	225	230	235	240
102	Asp Asp Gln Val Asp Arg Met Ala Asp Val Ser Arg Glu Ile Ser Ser			
103	245	250	255	
105	Val Ser Ala Ser Val Glu Glu Val Ala Ser Thr Ala Asp Asp Val Arg			
106	260	265	270	
108	Arg Thr Ser Glu Asp Ala Glu Ala Leu Ala Gln Gln Gly Glu Ala Ala			
109	275	280	285	
111	Ala Asp Asp Ala Leu Ala Thr Met Thr Asp Ile Asp Glu Ala Thr Asp			
112	290	295	300	
114	Gly Val Thr Ala Gly Val Glu Gln Leu Gly Glu Arg Ala Ala Asp Val			
115	305	310	315	320
117	Glu Ser Val Thr Gly Val Ile Asp Asp Ile Ala Glu Gln Thr Asn Met			
118	325	330	335	
120	Leu Ala Leu Asn Ala Ser Ile Glu Ala Ala Arg Ala Gly Glu Ala Gly			
121	340	345	350	
123	Glu Gly Phe Ala Val Val Ala Asp Glu Val Lys Ala Leu Ala Glu Glu			
124	355	360	365	
126	Ser Arg Glu Gln Ser Thr Arg Val Glu Glu Leu Val Glu Gln Met Gln			
127	370	375	380	
129	Ala Glu Thr Glu Glu Thr Val Asp Gln Leu Asp Glu Val Asn Gln Arg			
130	385	390	395	400
132	Ile Gly Glu Gly Val Glu Arg Val Glu Glu Ala Met Glu Thr Leu Gln			
133	405	410	415	

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001  
TIME: 13:15:00

Input Set : A:\H1020011.app  
Output Set: N:\CRF3\07062001\I455978.raw

135 Glu Ile Thr Asp Ala Val Glu Asp Ala Ala Ser Gly Met Gln Glu Val  
136 420 425 430  
138 Ser Thr Ala Thr Asp Glu Gln Ala Val Ser Thr Glu Glu Val Ala Glu  
139 435 440 445  
141 Met Val Asp Gly Val Asp Asp Arg Ala Gly Glu Ile Ala Ala Ala Leu  
142 450 455 460  
144 Asp Asp Ile Ala Asp Ala Thr Asp Gln Gln Val Arg Thr Val Glu Glu  
145 465 470 475 480  
147 Val Arg Glu Thr Val Gly Lys Leu Ser  
148 485  
151 <210> SEQ ID NO: 3  
152 <211> LENGTH: 1390  
153 <212> TYPE: DNA  
154 <213> ORGANISM: Bacillus subtilis  
156 <400> SEQUENCE: 3  
157 atgttattta aaaaagacag aaaacaagaa acagcttaact tttcagattc aaacggacaa 60  
158 caaaaaaacc gcattcagct cacaacacaa catcgatg tcaaaaaaca gctcaaaatg 120  
159 gtcaagggttgg gagatgctga gctttatgtt ttagagcagc ttcaagccact cattcaagaa 180  
160 aatatcgtaa atatcgtaa tgcttttat aaaaacctt accatgaaag ctcatgtatg 240  
161 gatatcatta atgatcacag ctcagttgac cgcttaaacaa acacgttaaa acggcatatt 300  
162 cagaaaatgt ttgcagcgt tatcgatgat gaatttattt aaaaagcgtaa ccgaatcgcc 360  
163 tccatccatt taagaatcgg ccttttgcua aatgttata tgggtgcgtt tcaagagctc 420  
164 cttttgtcaa tgattgacat ttatgaagcg tccattacaa atcagcaaga actgtaaaa 480  
165 gccattaaag caacaacaaa aatcttgaac tttagaacagc agcttgtcct tgaagcgttt 540  
166 caaagcgagt acaaccagac ccgtgatgaa caagaagaaa agaaaaaacct tcttcatcag 600  
167 aaaattcaag aaacctctgg atcgattgcc attctgttt cagaaacaag cagatcagtt 660  
168 caagagcttgg tggacaaatc tgaaggcatt tctcaagcat ccaaagccgg cactgtaaca 720  
169 tccagcactg ttgaagaaaa gtcgatcgcc ggaaaaaaaa agctagaagt ccagcaaaaa 780  
170 cagatgaaca aaattgacac aagccttgcc caaatcgaaa aagaaatggt caagctggat 840  
171 gaaatcgcc agcaaattga aaaaatcttc ggcattcgatca caggcatagc tgaacaaaca 900  
172 aaccttctct cgctcaatgc atctattgaa tccgcgcgc ccggagaaca cggcaaaggc 960  
173 ttgtgtcg tggcaaatga agtgcggaaat cttctgagg atacgaaaaa aaccgtctct 1020  
174 actgttctg agcttgatca caatacgaat acacaaatca acattgtatc caagcatatc 1080  
175 aaagacgtga atgagctagt cagcggaaatg aaagaaaaaa tgacgcaat taaccgttta 1140  
176 ttgcgtgaaa tcgtccacag catgaaaatc agcaaagagc aatcaggcaa aatcgacgtc 1200  
177 gatctgcaag ctttcttgg aggcttcag gaagtccatc ggcgcgttcc ccatgtggcc 1260  
178 gctccgttgg attcgcttgtt catcctgaca gaagaataac catcaaaaac cggctctgcca 1320  
179 tacggccgtt tttttgcgt tcattatgtt aacttaaatt aaaaatcagt tgacataata 1380  
180 attacgtca 1390  
183 <210> SEQ ID NO: 4  
184 <211> LENGTH: 432  
185 <212> TYPE: PRT  
186 <213> ORGANISM: Bacillus subtilis  
188 <400> SEQUENCE: 4  
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190 1 5 10 15  
192 Ser Asn Gly Gln Gln Lys Asn Arg Ile Gln Leu Thr Asn Lys His Ala  
193 20 25 30  
195 Asp Val Lys Lys Gln Leu Lys Met Val Arg Leu Gly Asp Ala Glu Leu

RAW SEQUENCE LISTING  
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Input Set : A:\H1020011.app  
Output Set: N:\CRF3\07062001\I455978.raw

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198	Tyr Val Leu Glu Gln Leu Gln Pro Leu Ile Gln Glu Asn Ile Val Asn			
199	50	55	60	
201	Ile Val Asp Ala Phe Tyr Lys Asn Leu Asp His Glu Ser Ser Leu Met			
202	65	70	75	80
204	Asp Ile Ile Asn Asp His Ser Ser Val Asp Arg Leu Lys Gln Thr Leu			
205	85	90	95	
207	Lys Arg His Ile Gln Glu Met Phe Ala Gly Val Ile Asp Asp Glu Phe			
208	100	105	110	
210	Ile Glu Lys Arg Asn Arg Ile Ala Ser Ile His Leu Arg Ile Gly Leu			
211	115	120	125	
213	Leu Pro Lys Trp Tyr Met Gly Ala Phe Gln Glu Leu Leu Leu Ser Met			
214	130	135	140	
216	Ile Asp Ile Tyr Glu Ala Ser Ile Thr Asn Gln Gln Glu Leu Leu Lys			
217	145	150	155	160
219	Ala Ile Lys Ala Thr Thr Lys Ile Leu Asn Leu Glu Gln Gln Leu Val			
220	165	170	175	
222	Leu Glu Ala Phe Gln Ser Glu Tyr Asn Gln Thr Arg Asp Glu Gln Glu			
223	180	185	190	
225	Glu Lys Lys Asn Leu Leu His Gln Lys Ile Gln Glu Thr Ser Gly Ser			
226	195	200	205	
228	Ile Ala Asn Leu Phe Ser Glu Thr Ser Arg Ser Val Gln Glu Leu Val			
229	210	215	220	
231	Asp Lys Ser Glu Gly Ile Ser Gln Ala Ser Lys Ala Gly Thr Val Thr			
232	225	230	235	240
234	Ser Ser Thr Val Glu Glu Lys Ser Ile Gly Gly Lys Lys Glu Leu Glu			
235	245	250	255	
237	Val Gln Gln Lys Gln Met Asn Lys Ile Asp Thr Ser Leu Val Gln Ile			
238	260	265	270	
240	Glu Lys Glu Met Val Lys Leu Asp Glu Ile Ala Gln Gln Ile Glu Lys			
241	275	280	285	
243	Ile Phe Gly Ile Val Thr Gly Ile Ala Glu Gln Thr Asn Leu Leu Ser			
244	290	295	300	
246	Leu Asn Ala Ser Ile Glu Ser Ala Arg Ala Gly Glu His Gly Lys Gly			
247	305	310	315	320
249	Phe Ala Val Val Ala Asn Glu Val Arg Lys Leu Ser Glu Asp Thr Lys			
250	325	330	335	
252	Lys Thr Val Ser Thr Val Ser Glu Leu Val Asn Asn Thr Asn Thr Gln			
253	340	345	350	
255	Ile Asn Ile Val Ser Lys His Ile Lys Asp Val Asn Glu Leu Val Ser			
256	355	360	365	
258	Glu Ser Lys Glu Lys Met Thr Gln Ile Asn Arg Leu Phe Asp Glu Ile			
259	370	375	380	
261	Val His Ser Met Lys Ile Ser Lys Glu Gln Ser Gly Lys Ile Asp Val			
262	385	390	395	400
264	Asp Leu Gln Ala Phe Leu Gly Gly Leu Gln Glu Val Ser Arg Ala Val			
265	405	410	415	
267	Ser His Val Ala Ala Ser Val Asp Ser Leu Val Ile Leu Thr Glu Glu			
268	420	425	430	

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001  
TIME: 13:15:00

Input Set : A:\H1020011.app  
Output Set: N:\CRF3\07062001\I455978.raw

274 <210> SEQ ID NO: 5  
 275 <211> LENGTH: 57  
 276 <212> TYPE: PRT  
 277 <213> ORGANISM: Artificial Sequence  
 279 <220> FEATURE:  
 280 <223> OTHER INFORMATION: Description of Artificial Sequence: Template  
 281 sequence  
 283 <220> FEATURE: *<222> must contain location of all Xaa's.*  
 284 <221> NAME/KEY: UNSURE *If Xaa's are all the same use of a range*  
 285 <222> LOCATION: (4) *to describe the location is fine. Sec item #8*  
*on Error*  
 286 <223> OTHER INFORMATION: X at any position in this sequence is unknown.  
 288 <400> SEQUENCE: 5  
 289 Ile Ile Lys Xaa Thr Val Pro Val Leu Xaa Glu His Gly Xaa Xaa Ile  
 290 1 5 10 15  
 292 Gly Gln Asp Val Leu Val Val Leu Ile Lys Xaa Asn Pro Glu Ile Gln  
 293 20 25 30  
 295 Glu Lys Phe Phe Phe Lys His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 296 35 40 45  
 298 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 299 50 55  
 302 <210> SEQ ID NO: 6  
 303 <211> LENGTH: 55  
 304 <212> TYPE: PRT  
 305 <213> ORGANISM: Erwinia chrysanthemi  
 307 <400> SEQUENCE: 6  
 308 Ile Lys Ser Thr Ile Pro Leu Leu Ala Glu Thr Gly Pro Ala Leu Thr  
 309 1 5 10 15  
 311 Ala His Phe Tyr Gln Arg Met Phe His His Asn Pro Glu Leu Lys Asp  
 312 20 25 30  
 314 Ile Phe Asn Met Ser Asn Gln Arg Asn Gly Asp Gln Arg Glu Ala Leu  
 315 35 40 45  
 317 Phe Asn Ala Ile Cys Ala Tyr  
 318 50 55  
 321 <210> SEQ ID NO: 7  
 322 <211> LENGTH: 56  
 323 <212> TYPE: PRT  
 324 <213> ORGANISM: Vitreoscilla stercoraria  
 326 <400> SEQUENCE: 7  
 327 Ile Ile Lys Ala Thr Val Pro Val Leu Lys Glu His Gly Val Thr Ile  
 328 1 5 10 15  
 330 Thr Thr Thr Phe Tyr Lys Asn Leu Phe Ala Lys His Pro Glu Val Arg  
 331 20 25 30  
 333 Pro Leu Phe Asp Met Gly Arg Gln Glu Ser Leu Glu Gln Pro Lys Ala  
 334 35 40 45  
 336 Leu Ala Met Thr Val Leu Ala Ala  
 337 50 55  
 340 <210> SEQ ID NO: 8  
 341 <211> LENGTH: 55  
 342 <212> TYPE: PRT

FYI:  
 Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001  
TIME: 13:15:01

Input Set : A:\H1020011.app  
Output Set: N:\CRF3\07062001\I455978.raw

L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:934 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42  
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50  
L:1700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82  
L:1703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82  
L:1722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83  
L:1744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84  
L:1763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85  
L:1785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86